We claim:

1. A method for identifying compounds that modulate topoisomerase activity, said method comprising:

a) providing cells expressing topoisomerase and containing a promoter sensitive to changes in DNA topology having a reporter gene operatively linked thereto;

b) measuring the expression of said reporter gene in the presence and in the absence of a test compound;

c) comparing the expression of said reporter gene in the presence of said compound with the expression in the absence of said compound; and

d) identifying a compound that modulates topoisomerase activity as one that yields an alteration in reporter gene expression in the presence of the compound relative to expression in the absence of the compound.

2. A method for identifying compounds that inhibit topoisomerase activity, said method comprising:

a) providing cells expressing topoisomerase and containing a promoter sensitive to changes in DNA topology having a reporter gene operatively linked thereto;

b) measuring the expression of said reporter gene in the presence and in the absence of a test compound;

c) comparing the expression of said reporter gene in the presence of said compound with the expression in the absence of said compound; and

d) identifying a compound that inhibits topoisomerase activity as one that yields an alteration in reporter gene expression in the presence of the compound relative to expression in the absence of the compound.

3. The method of claim 1 or 2, wherein the topoisomerase is a type II topoisomerase.

4. The method of claim 1 or 2, wherein the topoisomerase is a DNA gyrase.

5. The method of claim 1 or 2, wherein the topoisomerase is a recombinant topoisomerase.

6. The method of claim 1 or 2, wherein the topoisomerase is a prokaryotic, eukaryotic, or viral topoisomerase.

7. The method of claim 1 or 2, wherein the promoter is selected from *gyrA, gyrB, proU, tppB, ompC, ompF, topA, dnaA, hisD, recF, katE, katG, sodA, sodB, tonB,* and *lacIq* mutant, SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, and any functional fragment thereof.

8. The method of claim 1 or 2, wherein the cells are bacterial cells.

9. The method of claim 8, wherein the cells are Gram-positive bacterial cells.

10. The method of claim 8, wherein the cells are Gram-negative bacterial cells.

11. The method of claim 8, wherein the cells are selected from *Haemophilus influenzae, Moraxella catarrhalis, Pseudomonas aeruginosa, Escherichia coli, Chlamydia spp, Legionella spp, Staphylococcus aureus, Staphylococcus saprophyticus, Streptococcus pneumoniae, Streptococcus pyogenes, Streptococcus mutans, Enterococcus faecalis, Enterococcus faecium, Mycoplasma spp, Bacteroides spp* and *Clostridium spp.*

12. The method of claim 1 or 2, wherein the cells are eukaryotic cells selected from mammalian or fungal cells.

13. The method of claim 12, wherein the cells are human cells, *Saccharomyces spp, Aspergillus spp,* or *Candida spp* cells.

14. The method of claim 1 or 2, wherein the promoter and reporter gene are provided on a plasmid.

15. The method of claim 14, wherein the plasmid is a low copy plasmid.

16. The method of claim 14, wherein the plasmid is a medium copy plasmid.

17. The method of claim 14, wherein the plasmid is a high copy plasmid.

18. The method of claim 1 or 2, wherein the promoter and reporter gene are provided on a chromosome.

19. The method of claim 1 or 2, wherein the reporter gene is selected from *lacZ*, *luxABCDE* operon, *lucFF* operon, *luxAB* operon, *uidA*, *gfp*, *phoA*, *kan*, *cam*, and genes encoding reef coral fluorescent proteins.

20. The method of claim 1 or 2, wherein the reporter gene is *lacZ*.

21. The method of claim 1 or 2, wherein the reporter gene is the *luxABCDE* operon.

22. The method of claim 1 or 2, wherein the reporter gene is *ZsGreen1*.

23. A method for identifying compounds that modulate DNA gyrase activity, said method comprising:

a) providing cells expressing DNA gyrase and containing a promoter sensitive to changes in DNA topology having a reporter gene operatively linked thereto;

b) measuring the expression of said reporter gene in the presence and in the absence of a test compound; and

c) identifying a compound that modulates DNA gyrase activity as one that yields an alteration in reporter gene expression in the presence of the compound relative to expression in the absence of the compound.

24. A method for identifying compounds that inhibit DNA gyrase activity, said method comprising:

a) providing cells expressing DNA gyrase and containing a promoter sensitive to changes in DNA topology having a reporter gene operatively linked thereto;

b) measuring the expression of said reporter gene in the presence and in the absence of a test compound; and

c) identifying a compound that inhibits DNA gyrase activity as one that yields an alteration in reporter gene expression in the presence of the compound relative to expression in the absence of the compound.

25. The method of claim 23 or 24, wherein the DNA gyrase is a recombinant DNA gyrase.

26. The method of claim 23 or 24, wherein the DNA gyrase is selected from *Haemophilus influenzae, Moraxella catarrhalis, Pseudomonas aeruginosa, Escherichia coli, Chlamydia spp, Legionella spp, Staphylococcus aureus, Staphylococcus saprophyticus, Streptococcus pneumoniae, Streptococcus pyogenes, Streptococcus mutans, Enterococcus faecalis, Enterococcus faecium, Mycoplasma spp, Bacteroides spp* and *Clostridium spp*.

27. The method of claim 26 wherein the DNA gyrase is *E. coli* DNA gyrase.

28. The method of claim 26 wherein the DNA gyrase is *H. influenzae* DNA gyrase.

29. The method of claim 26 wherein the DNA gyrase is *S. aureus* DNA gyrase.

30. The method of claim 23 or 24, wherein the promoter is selected from *gyrA, gyrB, proU, tppB, ompC, ompF, topA, dnaA, hisD, recF, katE, katG, sodA, sodB, tonB*, and *lacIq* mutant, SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, and any functional fragment thereof.

31. The method of claim 23 or 24, wherein the cells are bacterial cells.

32. The method of claim 31, wherein the cells are Gram-positive bacterial cells.

33. The method of claim 31, wherein the cells are Gram-negative bacterial cells.

34. The method of claim 31, wherein the cells are selected from *Haemophilus influenzae, Moraxella catarrhalis, Pseudomonas aeruginosa, Escherichia coli, Chlamydia spp, Legionella spp, Staphylococcus aureus, Staphylococcus saprophyticus, Streptococcus*

pneumoniae, *Streptococcus pyogenes*, *Streptococcus mutans*, *Enterococcus faecalis*, *Enterococcus faecium*, *Mycoplasma spp*, *Bacteroides spp* and *Clostridium spp*.

35. The method of claim 23 or 24, wherein the cells are eukaryotic cells selected from mammalian or fungal cells.

36. The method of claim 35, wherein the cells are human cells, *Saccharomyces spp*, *Aspergillus spp*, or *Candida spp* cells.

37. The method of claim 23 or 24, wherein the promoter and reporter gene are provided on a plasmid.

38. The method of claim 37, wherein the plasmid is a low copy plasmid.

39. The method of claim 37, wherein the plasmid is a medium copy plasmid.

40. The method of claim 37, wherein the plasmid is a high copy plasmid.

41. The method of claim 23 or 24, wherein the promoter and reporter gene are provided on a chromosome.

42. The method of claim 23 or 24, wherein the reporter gene is selected from *lacZ*, *luxABCDE* operon, *lucFF* operon, *luxAB* operon, *uidA*, *gfp*, *phoA*, *kan*, *cam*, and genes encoding reef coral fluorescent proteins.

43. The method of claim 42, wherein the reporter gene is *lacZ*.

44. The method of claim 42, wherein the reporter gene is *luxABCDE* operon.

45. The method of claim 42, wherein the reporter gene is *ZsGreen1*.